



SEQUENCE LISTING

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<110> SYKEN, JOSH
MUNGER, KARL

<120> METHODS AND REAGENTS TO REGULATE APOPTOSIS

<130> HMV-054.01

<140> 09/908,992

<141> 2001-07-19

<150> 60/219,718

<151> 2000-07-19

<150> 60/219,537

<151> 2000-07-20

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<170> PatentIn Ver. 2.1

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Gly	Pro	Arg	Ala	Leu	Leu	Thr	Leu	Arg	Pro	Gly	Val	Ser	Leu	Thr	Gly	
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Thr	Lys	His	Asn	Pro	Phe	Ile	Cys	Thr	Ala	Ser	Phe	His	Thr	Ser	Ala	
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Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr
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Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln
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Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala
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Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp
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Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val
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cct	gtg	gga	aaa	agg	gaa	att	ttc	att	acg	ttc	agg	gtg	cag	aaa	agc	1008
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Tyr	Glu	Thr	Ile	Asn	Val	Thr	Ile	Pro	Pro	Gly	Thr	Gln	Thr	Asp	Gln	
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Lys	Ile	Arg	Met	Gly	Gly	Lys	Gly	Ile	Pro	Arg	Ile	Asn	Ser	Tyr	Gly	

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Asp Val Glu Gly	Thr Val Asn Gly	Val Thr Leu Thr	Ser Ser Gly Gly				
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agc acc atg gat	agc tcc gca gga	agc aag gct agg	cgt gag gct ggg	1392			
Ser Thr Met Asp	Ser Ser Ala Gly	Ser Lys Ala Arg	Arg Arg Glu Ala			Gly	
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Gly Val Val Gly	Ala Trp Leu Ser	Arg Lys Leu Ser	Val Pro Ala Phe				
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Ala Ser Ser Leu	Thr Ser Cys Gly	Pro Arg Ala Leu	Leu Leu Thr Arg				
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Pro Gly Val Ser	Leu Thr Gly Thr	Lys His Asn Pro	Phe Ile Cys Thr				
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Ala Ser Phe His	Thr Ser Ala Pro	Leu Ala Lys Glu	Asp Tyr Tyr Gln				
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Ile Leu Gly Val	Pro Arg Asn Ala	Ser Gln Lys Glu	Ile Lys Lys Ala				

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Tyr	Tyr	Gln	Leu	Ala	Lys	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp						
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Pro	Lys	Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val						
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Gly	Pro	Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu						
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ttc	tca	tcc	tct	tca	ttt	gga	gat	ttc	cag	acc	gtg	ttt	gat	cag	cct						624
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Gln	Glu	Tyr	Phe	Met	Glu	Leu	Thr	Phe	Asn	Gln	Ala	Ala	Lys	Gly	Val						
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Cys	Val	Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val						
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420 425 430

gat gtg gag ggg acg gtg aac ggc gtc acc ctc acc agc tct gga aaa 1344
Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Lys
435 440 445

aga tcc act gga aac tag 1362
Arg Ser Thr Gly Asn
450

<210> 4
<211> 1242
<212> DNA
<213> Homo sapiens

<400> 4
gtcagcctta caggaacaaa acataaccct ttcatttgta ctgcctcctt ccacacgagt 60
gccccttttg ccaaagaaga ttattatcag atattaggag tgcctcgaaa tgccagccag 120
aaagagatca agaaagccta ttatcagctt gccagaagt atcacctga cacaaataag 180
gatgatccca aagccaagga gaagttctcc cagctggcag aagcctatga ggttttgagt 240
gatgaggtga agaggaagca gtacgatgcc taaggctctg caggcttcga tcctggggcc 300
agcggctccc agcatagcta ctggaaggga ggccccactg tggaccccga ggagctgttc 360
aggaagatct ttggcgagtt ctcatcctct tcatttgag atttccagac cgtgtttgat 420
cagcctcagg aatacttcat ggagttgaca ttcaatcaag ctgcaaaggg ggtcaacaag 480
gagttcaccc tgaacatcat ggacacgtgt gagcgctgca acggcaaggg gaacgagccc 540
ggcaccaagg tgcagcattg ccaactactgt ggcggctccg gcatggaaac catcaacaca 600
ggcccttttg tgatgcgttc cacgtgtagg agatgtggtg gccgcggctc catcatcata 660
tcgccctgtg tggctctgcag gggagcagga caagccaagc agaaaaagcg agtgatgatc 720
cctgtgcctg caggagtcca ggatggccag accgtgagga tgcctgtggg aaaaaggga 780
attttcatta cgttcagggg gcagaaaagc cctgtgttcc ggagggacgg cgcagacatc 840
cactccgacc tctttatttc tatagctcag gctcttcttg ggggaacagc cagagcccag 900
ggcctgtacg agacgatcaa cgtgacgatc ccccttgga ctcagacaga ccagaagatt 960
cggatgggtg ggaaaggcat ccccggatt aacagctacg gctacggaga ccaactacatc 1020
cacatcaaga tacgagttcc aaagaggcta acgagccggc agcagagcct gatcctgagc 1080
tacgccgagg acgagacaga tgtggagggg acggtgaacg gcgtcaccct caccagctct 1140
ggtggcagca ccatggatag ctccgcagga agcaaggcta ggcgtgaggc tggggaggac 1200
gaggagggat tcctttccaa acttaagaaa atgtttacct ca 1242

<210> 5
<211> 1161

<212> DNA
<213> Homo sapiens

<400> 5
gtcagcctta caggaacaaa acataaccct ttcatttgta ctgcctcctt ccacacgagt 60
gccccctttgg ccaaagaaga ttattatcag atattaggag tgcctcgaaa tgccagccag 120
aaagagatca agaaagccta ttatcagctt gccaaagaag atcaccttga cacaataaag 180
gatgatccca aagccaagga gaagttctcc cagctggcag aagcctatga ggttttgagt 240
gatgaggtga agaggaagca gtacgatgcc tacggctctg caggcttcga tcctggggcc 300
agcggctccc agcatagcta ctggaagggg gggccctactg tggaccccga ggagctgttc 360
aggaagatct ttggcgagtt ctcatcctct tcatttggag atttccagac cgtgtttgat 420
cagcctcagg aatacttcat ggagttgaca ttcaatcaag ctgcaaaggg ggtcaacaag 480
gagttcacccg tgaacatcat ggacacgtgt gagcgctgca acggcaaggg gaacgagccc 540
ggcaccaagg tgcagcattg ccactactgt ggcggctccg gcatggaaac catcaacaca 600
ggcccttttg tgatgcgttc cacgtgtagg agatgtggtg gccgcggctc catcatcata 660
tcgccctgtg tggctctgcag gggagcagga caagccaagc agaaaaagcg agtgatgatc 720
cctgtgcctg caggagtcga ggatggccag accgtgagga tgctgtgtgg aaaaagggaa 780
attttcatta cgttcagggt gcagaaaagc cctgtgttcc ggagggacgg cgagacatc 840
cactccgacc tctttatttc tatagctcag gctcttcttg ggggaacagc cagagcccag 900
ggcctgtacg agacgatcaa cgtgacgac cccctggga ctcagacaga ccagaagatt 960
cggatgggtg ggaaaggcat ccccggatt aacagctacg gctacggaga cactacatc 1020
cacatcaaga tacgagttcc aaagaggcta acgagccggc agcagagcct gatcctgagc 1080
tacgccgagg acgagacaga tgtggagggg acggtgaacg gcgtcaccct caccagctct 1140
ggaaaaagat ccactggaaa c 1161

<210> 6
<211> 99
<212> DNA
<213> Homo sapiens

<400> 6
ggcagcacca tggatagctc cgcaggaagc aaggctaggc gtgaggctgg ggaggacgag 60
gagggattcc tttccaaact taagaaaatg tttacctca 99

<210> 7
<211> 18
<212> DNA
<213> Homo sapiens

<400> 7
aaaagatcca ctggaaac 18

<210> 8
<211> 480
<212> PRT
<213> Homo sapiens

<400> 8
Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr
1 5 10 15
Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu
20 25 30
Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe
35 40 45
Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg

50					55					60					
Pro	Gly	Val	Ser	Leu	Thr	Gly	Thr	Lys	His	Asn	Pro	Phe	Ile	Cys	Thr
65					70					75					80
Ala	Ser	Phe	His	Thr	Ser	Ala	Pro	Leu	Ala	Lys	Glu	Asp	Tyr	Tyr	Gln
				85					90					95	
Ile	Leu	Gly	Val	Pro	Arg	Asn	Ala	Ser	Gln	Lys	Glu	Ile	Lys	Lys	Ala
			100					105					110		
Tyr	Tyr	Gln	Leu	Ala	Lys	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp
		115					120					125			
Pro	Lys	Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val
	130					135					140				
Leu	Ser	Asp	Glu	Val	Lys	Arg	Lys	Gln	Tyr	Asp	Ala	Tyr	Gly	Ser	Ala
145					150					155					160
Gly	Phe	Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly
				165					170					175	
Gly	Pro	Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu
			180					185					190		
Phe	Ser	Ser	Ser	Ser	Phe	Gly	Asp	Phe	Gln	Thr	Val	Phe	Asp	Gln	Pro
		195					200					205			
Gln	Glu	Tyr	Phe	Met	Glu	Leu	Thr	Phe	Asn	Gln	Ala	Ala	Lys	Gly	Val
	210					215					220				
Asn	Lys	Glu	Phe	Thr	Val	Asn	Ile	Met	Asp	Thr	Cys	Glu	Arg	Cys	Asn
225					230					235					240
Gly	Lys	Gly	Asn	Glu	Pro	Gly	Thr	Lys	Val	Gln	His	Cys	His	Tyr	Cys
			245						250					255	
Gly	Gly	Ser	Gly	Met	Glu	Thr	Ile	Asn	Thr	Gly	Pro	Phe	Val	Met	Arg
			260					265					270		
Ser	Thr	Cys	Arg	Arg	Cys	Gly	Gly	Arg	Gly	Ser	Ile	Ile	Ile	Ser	Pro
		275					280					285			
Cys	Val	Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val
	290					295					300				
Met	Ile	Pro	Val	Pro	Ala	Gly	Val	Glu	Asp	Gly	Gln	Thr	Val	Arg	Met
305					310					315					320
Pro	Val	Gly	Lys	Arg	Glu	Ile	Phe	Ile	Thr	Phe	Arg	Val	Gln	Lys	Ser
				325					330				335		
Pro	Val	Phe	Arg	Arg	Asp	Gly	Ala	Asp	Ile	His	Ser	Asp	Leu	Phe	Ile
			340				345						350		
Ser	Ile	Ala	Gln	Ala	Leu	Leu	Gly	Gly	Thr	Ala	Arg	Ala	Gln	Gly	Leu
		355					360					365			
Tyr	Glu	Thr	Ile	Asn	Val	Thr	Ile	Pro	Pro	Gly	Thr	Gln	Thr	Asp	Gln
	370					375					380				

Lys Ile Arg Met Gly Gly Lys Gly Ile Pro Arg Ile Asn Ser Tyr Gly
385 390 395 400

Tyr Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu
405 410 415

Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr
420 425 430

Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Gly
435 440 445

Ser Thr Met Asp Ser Ser Ala Gly Ser Lys Ala Arg Arg Glu Ala Gly
450 455 460

Glu Asp Glu Glu Gly Phe Leu Ser Lys Leu Lys Lys Met Phe Thr Ser
465 470 475 480

<210> 9

<211> 453

<212> PRT

<213> Homo sapiens

<400> 9

Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr
1 5 10 15

Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu
20 25 30

Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe
35 40 45

Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg
50 55 60

Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr
65 70 75 80

Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln
85 90 95

Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala
100 105 110

Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp
115 120 125

Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val
130 135 140

Leu Ser Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala
145 150 155 160

Gly Phe Asp Pro Gly Ala Ser Gly Ser Gln His Ser Tyr Trp Lys Gly
165 170 175

Gly Pro Thr Val Asp Pro Glu Glu Leu Phe Arg Lys Ile Phe Gly Glu
180 185 190

Phe Ser Ser Ser Ser Phe Gly Asp Phe Gln Thr Val Phe Asp Gln Pro
195 200 205

Gln Glu Tyr Phe Met Glu Leu Thr Phe Asn Gln Ala Ala Lys Gly Val
210 215 220

Asn Lys Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asn
225 230 235 240

Gly Lys Gly Asn Glu Pro Gly Thr Lys Val Gln His Cys His Tyr Cys
245 250 255

Gly Gly Ser Gly Met Glu Thr Ile Asn Thr Gly Pro Phe Val Met Arg
260 265 270

Ser Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Ile Ser Pro
275 280 285

Cys Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val
290 295 300

Met Ile Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met
305 310 315 320

Pro Val Gly Lys Arg Glu Ile Phe Ile Thr Phe Arg Val Gln Lys Ser
325 330 335

Pro Val Phe Arg Arg Asp Gly Ala Asp Ile His Ser Asp Leu Phe Ile
340 345 350

Ser Ile Ala Gln Ala Leu Leu Gly Gly Thr Ala Arg Ala Gln Gly Leu
355 360 365

Tyr Glu Thr Ile Asn Val Thr Ile Pro Pro Gly Thr Gln Thr Asp Gln
370 375 380

Lys Ile Arg Met Gly Gly Lys Gly Ile Pro Arg Ile Asn Ser Tyr Gly
385 390 395 400

Tyr Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu
405 410 415

Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr
420 425 430

Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Lys
435 440 445

Arg Ser Thr Gly Asn
450

<210> 10

<211> 414

<212> PRT

<213> Homo sapiens

<400> 10

Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr Ala Ser
1 5 10 15

Phe	His	Thr	Ser	Ala	Pro	Leu	Ala	Lys	Glu	Asp	Tyr	Tyr	Gln	Ile	Leu	20	25	30
Gly	Val	Pro	Arg	Asn	Ala	Ser	Gln	Lys	Glu	Ile	Lys	Lys	Ala	Tyr	Tyr	35	40	45
Gln	Leu	Ala	Lys	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp	Pro	Lys	50	55	60
Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val	Leu	Ser	65	70	75
Asp	Glu	Val	Lys	Arg	Lys	Gln	Tyr	Asp	Ala	Tyr	Gly	Ser	Ala	Gly	Phe	85	90	95
Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly	Gly	Pro	100	105	110
Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu	Phe	Ser	115	120	125
Ser	Ser	Ser	Phe	Gly	Asp	Phe	Gln	Thr	Val	Phe	Asp	Gln	Pro	Gln	Glu	130	135	140
Tyr	Phe	Met	Glu	Leu	Thr	Phe	Asn	Gln	Ala	Ala	Lys	Gly	Val	Asn	Lys	145	150	155
Glu	Phe	Thr	Val	Asn	Ile	Met	Asp	Thr	Cys	Glu	Arg	Cys	Asn	Gly	Lys	165	170	175
Gly	Asn	Glu	Pro	Gly	Thr	Lys	Val	Gln	His	Cys	His	Tyr	Cys	Gly	Gly	180	185	190
Ser	Gly	Met	Glu	Thr	Ile	Asn	Thr	Gly	Pro	Phe	Val	Met	Arg	Ser	Thr	195	200	205
Cys	Arg	Arg	Cys	Gly	Gly	Arg	Gly	Ser	Ile	Ile	Ile	Ser	Pro	Cys	Val	210	215	220
Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val	Met	Ile	225	230	235
Pro	Val	Pro	Ala	Gly	Val	Glu	Asp	Gly	Gln	Thr	Val	Arg	Met	Pro	Val	245	250	255
Gly	Lys	Arg	Glu	Ile	Phe	Ile	Thr	Phe	Arg	Val	Gln	Lys	Ser	Pro	Val	260	265	270
Phe	Arg	Arg	Asp	Gly	Ala	Asp	Ile	His	Ser	Asp	Leu	Phe	Ile	Ser	Ile	275	280	285
Ala	Gln	Ala	Leu	Leu	Gly	Gly	Thr	Ala	Arg	Ala	Gln	Gly	Leu	Tyr	Glu	290	295	300
Thr	Ile	Asn	Val	Thr	Ile	Pro	Pro	Gly	Thr	Gln	Thr	Asp	Gln	Lys	Ile	305	310	315
Arg	Met	Gly	Gly	Lys	Gly	Ile	Pro	Arg	Ile	Asn	Ser	Tyr	Gly	Tyr	Gly	325	330	335

Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu Thr Ser
340 345 350

Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr Asp Val
355 360 365

Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Gly Ser Thr
370 375 380

Met Asp Ser Ser Ala Gly Ser Lys Ala Arg Arg Glu Ala Gly Glu Asp
385 390 395 400

Glu Glu Gly Phe Leu Ser Lys Leu Lys Lys Met Phe Thr Ser
405 410

<210> 11
<211> 387
<212> PRT
<213> Homo sapiens

<400> 11
Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr Ala Ser
1 5 10 15

Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln Ile Leu
20 25 30

Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala Tyr Tyr
35 40 45

Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp Pro Lys
50 55 60

Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val Leu Ser
65 70 75 80

Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala Gly Phe
85 90 95

Asp Pro Gly Ala Ser Gly Ser Gln His Ser Tyr Trp Lys Gly Gly Pro
100 105 110

Thr Val Asp Pro Glu Glu Leu Phe Arg Lys Ile Phe Gly Glu Phe Ser
115 120 125

Ser Ser Ser Phe Gly Asp Phe Gln Thr Val Phe Asp Gln Pro Gln Glu
130 135 140

Tyr Phe Met Glu Leu Thr Phe Asn Gln Ala Ala Lys Gly Val Asn Lys
145 150 155 160

Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asn Gly Lys
165 170 175

Gly Asn Glu Pro Gly Thr Lys Val Gln His Cys His Tyr Cys Gly Gly
180 185 190

Ser Gly Met Glu Thr Ile Asn Thr Gly Pro Phe Val Met Arg Ser Thr
195 200 205

Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Ile Ser Pro Cys Val
 210 215 220
 Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val Met Ile
 225 230 235 240
 Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met Pro Val
 245 250 255
 Gly Lys Arg Glu Ile Phe Ile Thr Phe Arg Val Gln Lys Ser Pro Val
 260 265 270
 Phe Arg Arg Asp Gly Ala Asp Ile His Ser Asp Leu Phe Ile Ser Ile
 275 280 285
 Ala Gln Ala Leu Leu Gly Gly Thr Ala Arg Ala Gln Gly Leu Tyr Glu
 290 295 300
 Thr Ile Asn Val Thr Ile Pro Pro Gly Thr Gln Thr Asp Gln Lys Ile
 305 310 315 320
 Arg Met Gly Gly Lys Gly Ile Pro Arg Ile Asn Ser Tyr Gly Tyr Gly
 325 330 335
 Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu Thr Ser
 340 345 350
 Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr Asp Val
 355 360 365
 Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Lys Arg Ser
 370 375 380
 Thr Gly Asn
 385

<210> 12
 <211> 480
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr
 1 5 10 15
 Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu
 20 25 30
 Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe
 35 40 45
 Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg
 50 55 60
 Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr
 65 70 75 80
 Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln
 85 90 95

Ile	Leu	Gly	Val	Pro	Arg	Asn	Ala	Ser	Gln	Lys	Glu	Ile	Lys	Lys	Ala	100	105	110	
Tyr	Tyr	Gln	Leu	Ala	Lys	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp	115	120	125	
Pro	Lys	Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val	130	135	140	
Leu	Ser	Asp	Glu	Val	Lys	Arg	Lys	Gln	Tyr	Asp	Ala	Tyr	Gly	Ser	Ala	145	150	155	160
Gly	Phe	Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly	165	170	175	
Gly	Pro	Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu	180	185	190	
Phe	Ser	Ser	Ser	Ser	Phe	Gly	Asp	Phe	Gln	Thr	Val	Phe	Asp	Gln	Pro	195	200	205	
Gln	Glu	Tyr	Phe	Met	Glu	Leu	Thr	Phe	Asn	Gln	Ala	Ala	Lys	Gly	Val	210	215	220	
Asn	Lys	Glu	Phe	Thr	Val	Asn	Ile	Met	Asp	Thr	Cys	Glu	Arg	Cys	Asn	225	230	235	240
Gly	Lys	Gly	Asn	Glu	Pro	Gly	Thr	Lys	Val	Gln	His	Cys	His	Tyr	Cys	245	250	255	
Gly	Gly	Ser	Gly	Met	Glu	Thr	Ile	Asn	Thr	Gly	Pro	Phe	Val	Met	Arg	260	265	270	
Ser	Thr	Cys	Arg	Arg	Cys	Gly	Gly	Arg	Gly	Ser	Ile	Ile	Ile	Ser	Pro	275	280	285	
Cys	Val	Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val	290	295	300	
Met	Ile	Pro	Val	Pro	Ala	Gly	Val	Glu	Asp	Gly	Gln	Thr	Val	Arg	Met	305	310	315	320
Pro	Val	Gly	Lys	Arg	Glu	Ile	Phe	Ile	Thr	Phe	Arg	Val	Gln	Lys	Ser	325	330	335	
Pro	Val	Phe	Arg	Arg	Asp	Gly	Ala	Asp	Ile	His	Ser	Asp	Leu	Phe	Ile	340	345	350	
Ser	Ile	Ala	Gln	Ala	Leu	Leu	Gly	Gly	Thr	Ala	Arg	Ala	Gln	Gly	Leu	355	360	365	
Tyr	Glu	Thr	Ile	Asn	Val	Thr	Ile	Pro	Pro	Gly	Thr	Gln	Thr	Asp	Gln	370	375	380	
Lys	Ile	Arg	Met	Gly	Gly	Lys	Gly	Ile	Pro	Arg	Ile	Asn	Ser	Tyr	Gly	385	390	395	400
Tyr	Gly	Asp	His	Tyr	Ile	His	Ile	Lys	Ile	Arg	Val	Pro	Lys	Arg	Leu	405	410	415	
Thr	Ser	Arg	Gln	Gln	Ser	Leu	Ile	Leu	Ser	Tyr	Ala	Glu	Asp	Glu	Thr				

420	425	430
Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Gly		
435	440	445
Ser Thr Met Asp Ser Ser Ala Gly Ser Lys Ala Arg Arg Glu Ala Gly		
450	455	460
Glu Asp Glu Glu Gly Phe Leu Ser Lys Leu Lys Lys Met Phe Thr Ser		
465	470	475 480

<210> 13
 <211> 33
 <212> PRT
 <213> Homo sapiens

<400> 13
 Gly Ser Thr Met Asp Ser Ser Ala Gly Ser Lys Ala Arg Arg Glu Ala
 1 5 10 15
 Gly Glu Asp Glu Glu Gly Phe Leu Ser Lys Leu Lys Lys Met Phe Thr
 20 25 30

Ser

<210> 14
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 14
 Lys Arg Ser Thr Gly Asn
 1 5

<210> 15
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 15
 Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys Arg
 1 5 10 15

Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser
 20 25

<210> 16
 <211> 12
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: EGF derived

peptide

<400> 16

Cys Met His Ile Glu Ser Leu Asp Ser Tyr Thr Cys
1 5 10

<210> 17

<211> 12

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: EGF derived
peptide

<400> 17

Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys
1 5 10

<210> 18

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
internalizing peptide

<400> 18

Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu
1 5 10 15

Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala
20 25

<210> 19

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative
peptide

<400> 19

Gly Asn Ala Ala Ala Ala Arg Arg
1 5

<210> 20

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 20

cgagacagat gtggagggga

20

<210> 21

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 21

gaataattta aacacact

18

<210> 22

<211> 36

<212> PRT

<213> Homo sapiens

<400> 22

Ser Ser Gly Gly Ser Thr Met Asp Ser Ser Ala Gly Ser Lys Ala Arg
1 5 10 15

Arg Glu Ala Gly Glu Asp Glu Glu Gly Phe Leu Ser Lys Leu Lys Lys
20 25 30

Met Phe Thr Ser
35

<210> 23

<211> 9

<212> PRT

<213> Homo sapiens

<400> 23

Ser Ser Gly Lys Arg Ser Thr Gly Asn
1 5

<210> 24

<211> 33

<212> PRT

<213> Homo sapiens

<400> 24

Gly Ser Thr Met Asp Ser Ser Ala Gly Ser Lys Ala Arg Arg Glu Ala
1 5 10 15

Gly Glu Asp Glu Glu Gly Phe Leu Ser Lys Leu Lys Lys Met Phe Thr
20 25 30

Ser

<210> 25

<211> 33

<212> PRT

<213> Mus sp.

<400> 25

Gly Arg Thr Met Asp Ser Ser Ala Glu Ser Lys Asp Arg Arg Glu Ala
1 5 10 15

Gly Glu Asp Asn Glu Gly Phe Leu Ser Lys Leu Lys Lys Ile Phe Thr
20 25 30

Ser

<210> 26

<211> 6

<212> PRT

<213> Homo sapiens

<400> 26

Lys Arg Ser Thr Gly Asn
1 5

<210> 27

<211> 6

<212> PRT

<213> Mus sp.

<400> 27

Lys Arg Ser Thr Gly Asn
1 5

<210> 28

<211> 479

<212> PRT

<213> Mus sp.

<220>

<221> MOD_RES

<222> (206)..(224)

<223> Unknown amino acid

<400> 28

Met Ala Ala Trp Cys Ser Pro Arg Trp Leu Arg Val Ala Val Gly Thr
1 5 10 15

Pro Arg Leu Pro Ala Ala Ala Gly Arg Gly Val Gln Gln Pro Gln Gly
20 25 30

Gly Val Val Ala Thr Ser Leu Cys Arg Lys Leu Cys Val Ser Ala Phe
35 40 45

Gly Leu Ser Met Gly Ala His Gly Pro Arg Ala Leu Leu Thr Leu Arg
50 55 60

Pro Gly Val Arg Leu Thr Gly Thr Lys Ser Phe Pro Phe Val Cys Thr
65 70 75 80

Thr Ser Phe His Thr Ser Ala Ser Leu Ala Lys Asp Asp Tyr Tyr Gln
85 90 95

Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Asp Ile Lys Lys Ala
100 105 110

Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp
115 120 125

Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val
130 135 140

Leu Ser Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala
145 150 155 160

Gly Phe Asp Pro Gly Thr Ser Ser Ser Gly Gln Gly Tyr Trp Arg Gly
165 170 175

Gly Pro Ser Val Asp Pro Glu Glu Leu Phe Arg Lys Ile Phe Gly Glu
180 185 190

Phe Ser Ser Ser Pro Phe Gly Asp Phe Gln Asn Val Val Xaa Xaa Xaa
195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
210 215 220

Lys Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asp Gly
225 230 235 240

Lys Gly Asn Glu Pro Gly Thr Lys Val Gln His Cys His Tyr Cys Gly
245 250 255

Gly Ser Gly Met Glu Thr Ile Asn Thr Gly Pro Phe Val Met Arg Ser
260 265 270

Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Thr Asn Pro Cys
275 280 285

Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val Thr
290 295 300

Ile Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met Pro
305 310 315 320

Val Gly Lys Arg Glu Ile Phe Val Thr Phe Arg Val Gln Lys Ser Pro
325 330 335

Val Phe Arg Arg Thr Cys Ala Asp Ile His Ser Asp Leu Phe Ile Ser
340 345 350

Ile Ala Gln Ala Ile Leu Gly Gly Thr Ala Lys Ala Gln Gly Leu Tyr
355 360 365

Glu Thr Ile Asn Val Thr Ile Pro Ala Gly Ile Gln Thr Asp Gln Lys
370 375 380

Ile Arg Leu Thr Gly Lys Gly Ile Pro Arg Ile Asn Ser Tyr Gly Tyr
385 390 395 400

Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu Ser
405 410 415

Ser Arg Gln Gln Asn Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr Asp
420 425 430

Val Glu Gly Thr Val Asn Gly Val Thr His Thr Ser Thr Gly Gly Arg
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Thr Met Asp Ser Ser Ala Glu Ser Lys Asp Arg Arg Glu Ala Gly Glu
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Gly Val Val Ala Thr Ser Leu Cys Arg Lys Leu Cys Val Ser Ala Phe
35 40 45
Gly Leu Ser Met Gly Ala His Gly Pro Arg Ala Leu Leu Thr Leu Arg
50 55 60
Pro Gly Val Arg Leu Thr Gly Thr Lys Ser Phe Pro Phe Val Cys Thr
65 70 75 80
Thr Ser Phe His Thr Ser Ala Ser Leu Ala Lys Asp Asp Tyr Tyr Gln
85 90 95
Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Asp Ile Lys Lys Ala
100 105 110
Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp
115 120 125
Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val
130 135 140
Leu Ser Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala
145 150 155 160
Gly Phe Asp Pro Gly Thr Ser Ser Ser Gly Gln Gly Tyr Trp Arg Gly
165 170 175
Gly Pro Ser Val Asp Pro Glu Glu Leu Phe Arg Lys Ile Phe Gly Glu
180 185 190
Phe Ser Ser Ser Pro Phe Gly Asp Phe Gln Asn Val Val Xaa Xaa Xaa
195 200 205
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

210	215	220
Lys Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asp Gly		
225	230	235 240
Lys Gly Asn Glu Pro Gly Thr Lys Val Gln His Cys His Tyr Cys Gly		
	245	250 255
Gly Ser Gly Met Glu Thr Ile Asn Thr Gly Pro Phe Val Met Arg Ser		
	260	265 270
Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Thr Asn Pro Cys		
	275	280 285
Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val Thr		
	290	295 300
Ile Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met Pro		
305	310	315 320
Val Gly Lys Arg Glu Ile Phe Val Thr Phe Arg Val Gln Lys Ser Pro		
	325	330 335
Val Phe Arg Arg Thr Cys Ala Asp Ile His Ser Asp Leu Phe Ile Ser		
	340	345 350
Ile Ala Gln Ala Ile Leu Gly Gly Thr Ala Lys Ala Gln Gly Leu Tyr		
	355	360 365
Glu Thr Ile Asn Val Thr Ile Pro Ala Gly Ile Gln Thr Asp Gln Lys		
	370	375 380
Ile Arg Leu Thr Gly Lys Gly Ile Pro Arg Ile Asn Ser Tyr Gly Tyr		
385	390	395 400
Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu Ser		
	405	410 415
Ser Arg Gln Gln Asn Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr Asp		
	420	425 430
Val Glu Gly Thr Val Asn Gly Val Thr His Thr Ser Thr Gly Lys Arg		
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Ser Thr Gly Asn		
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Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr		
1	5	10 15
Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu		
	20	25 30

Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe
35 40 45

Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg
50 55 60

Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr
65 70 75 80

Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln
85 90 95

Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala
100 105 110

Tyr Tyr Gln Leu Ala Lys Lys Tyr Gln Pro Asp Thr Asn Lys Asp Asp
115 120 125

Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val
130 135 140

Leu Ser Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala
145 150 155 160

Gly Phe Asp Pro Gly Ala Ser Gly Ser Gln His Ser Tyr Trp Lys Gly
165 170 175

Gly Pro Thr Val Asp Pro Glu Glu Leu Phe Arg Lys Ile Phe Gly Glu
180 185 190

Phe Ser Ser Ser Ser Phe Gly Asp Phe Gln Thr Val Phe Asp Gln Pro
195 200 205

Gln Glu Tyr Phe Met Glu Leu Thr Phe Asn Gln Ala Ala Lys Gly Val
210 215 220

Asn Lys Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asn
225 230 235 240

Gly Lys Gly Asn Glu Pro Gly Thr Lys Val Gln His Cys His Tyr Cys
245 250 255

Gly Gly Ser Gly Met Glu Thr Ile Asn Thr Gly Pro Phe Val Met Arg
260 265 270

Ser Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Ile Ser Pro
275 280 285

Cys Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val
290 295 300

Met Ile Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met
305 310 315 320

Pro Val Gly Lys Arg Glu Ile Phe Ile Thr Phe Arg Val Gln Lys Ser
325 330 335

Pro Val Phe Arg Arg Asp Gly Ala Asp Ile His Ser Asp Leu Phe Ile
340 345 350

Ser Ile Ala Gln Ala Leu Leu Gly Gly Thr Ala Arg Ala Gln Gly Leu
355 360 365

Tyr Glu Thr Ile Asn Val Thr Ile Pro Pro Gly Thr Gln Thr Asp Gln
370 375 380

Lys Ile Arg Met Gly Gly Lys Gly Ile Pro Arg Ile Asn Ser Tyr Gly
385 390 395 400

Tyr Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu
405 410 415

Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr
420 425 430

Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Lys
435 440 445

Arg Ser Thr Gly Asn
450